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FILE LAST UPDATED: 5 Nov 2002 (20021105/ED)

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=> s (dna# and microarray#)/bi,ab 585159 DNA#/BI 478773 DNA#/AB 9336 MICROARRAY#/BI 4308 MICROARRAY#/AB
L1 7117 (DNA# AND MICROARRAY#)/BI,AB

=> s bacteri?/bi,ab 477036 BACTERI?/BI 348680 BACTERI?/AB
L2 477036 BACTERI?/BI,AB

=> s (strain (5w) identif?)/bi,ab 330192 STRAIN/BI 300002 STRAIN/AB 781142 IDENTIF?/BI 714069 IDENTIF?/AB
L3 2439 (STRAIN (5W) IDENTIF?)/BI,AB

=> s (strain (5a) indentif?)/bi,ab 330192 STRAIN/BI 300002 STRAIN/AB 1385 INDENTIF?/BI 825 INDENTIF?/AB
L4 7 (STRAIN (5A) INDENTIF?)/BI,AB

=> s (strain (5a) identif?)/bi,ab 330192 STRAIN/BI 300002 STRAIN/AB 781142 IDENTIF?/BI 714069 IDENTIF?/AB
L5 3704 (STRAIN (5A) IDENTIF?)/BI,AB

=> s (listeria or monocytogenes or escherichia or coli)/bi,ab 5787 LISTERIA/BI 4268 LISTERIA/AB 4998 MONOCYTOGENES/BI 4258 MONOCYTOGENES/AB 207488 ESCHERICHIA/BI 134595 ESCHERICHIA/AB 224505 COLI/BI 196155 COLI/AB
L6 230844 (LISTERIA OR MONOCYTOGENES OR ESCHERICHIA OR COLI)/BI,AB

=> s (lactobacillus or casei or lactus or salmonella)/bi,ab 17585 LACTOBACILLUS/BI 12387 LACTOBACILLUS/AB 4414 CASEI/BI 3838 CASEI/AB 28 LACTUS/BI 10 LACTUS/AB 36073 SALMONELLA/BI 26548 SALMONELLA/AB
L7 53573 (LACTOBACILLUS OR CASEI OR LACTUS OR SALMONELLA)/BI,AB

=> s (typhimurium or enereditis or typhi)/bi,ab 19561
TYPHIMURIUM/BI 16660 TYPHIMURIUM/AB 0 ENEREDITIS/BI
0 ENEREDITIS/AB 3374 TYPHI/BI 2355 TYPHI/AB
L8 22491 (TYPHIMURIUM OR ENEREDITIS OR TYPHI)/BI,AB

=> s entereditis/bi,ab 0 ENTEREDITIS/BI 0 ENTEREDITIS/AB
L9 0 ENTEREDITIS/BI,AB

=> s l6 or l7 or l8
L10 271872 L6 OR L7 OR L8

=> s l2 or l10
L11 651789 L2 OR L10

=> s l1 and l11
L12 1267 L1 AND L11

=> s l5 and l12

L13 3 L5 AND L12

=> d l13 1-3 bib ab

L13 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2002 ACS
AN 2002:429085 CAPLUS
DN 137:1573
TI ***Lactobacillus*** rhamnosus polynucleotides, polypeptides and methods for their use
IN Glenn, Matthew; Havukkala, Ilkka J.; Lubbers, Mark William; Dekker, James
PA Genesis Research and Development Corporation Limited, N. Z.; Vialactia Bioscience (NZ) Limited
SO PCT Int. Appl., 128 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 6 PATENT NO. KIND DATE APPLICATION NO. DATE ----
---------- ---- -------- ---------- --------
PI WO 2002044383 A1 20020606 WO 2001-NZ286 20011128 W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 6476209 B1 20021105 US 2000-724623 20001128 AU 2002016499 A5 20020611 AU 2002-16499 20011128 US 2002151063 A1 20021017 US 2001-28415 20011220
PRAI US 2000-724623 A 20001128 US 1996-713557 A2 19960830 US 1998-36004 B2 19980304 US 2000-724809 A2 20001128 WO 2001-NZ286 W 20011128
AB Fifty-nine novel polynucleotides isolated from ***Lactobacillus*** rhamnosus are disclosed, as well as probes and primers, genetic constructs comprising the polynucleotides, biol. materials, including plants, microorganisms and multicellular organisms incorporating the polynucleotides, polypeptides expressed by the polynucleotides, and methods for using the polynucleotides and polypeptides. The polynucleotides were isolated by high-throughput sequencing of ***DNA*** libraries from the lactic acid ***bacteria*** L. rhamnosus ***strain*** HN001, and ***identified*** by comparison and alignment with known sequences in the public databases. The polynucleotides and polypeptides have use as enzyme activities, anti-infective activities, fermentative prodn. of useful products, immune system modulating activity, dairy product manuf.,adhesion activity, and regulatory activity.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2002 ACS
AN 2002:220823 CAPLUS
DN 136:261809
TI Identifying T cell and antigen recognition epitopes by positional scanning synthetic combinatorial libraries and artificial neural network
IN Martin, Roland; Simon, Richard; Zhao, Yingdong; Gran, Bruno; Pinilla, Clemencia
PA United States, Department of Health and Human Services, USA
SO PCT Int. Appl., 97 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ----
---------- ---- -------- ---------- --------
PI WO 2002022860 A2 20020321 WO 2001-US42166 20010911 W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EC, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2001093281 A5 20020326 AU 2001-93281 20010911
PRAI US 2000-232101P P 20000912 US 2000-251216P P 20001129 WO 2001-US42166 W 20010911
AB Described is a system and method comprises positional scanning synthetic combinatorial libraries or PS-SCL, artificial neural network, cDNA ***microarray*** anal., and RT-PCR-single strand conformation polymorphism for identifying T cell and other epitopes and the like. Thus, proliferative response of T cell clones GP5F11 (specific for influenza virus hemagglutinin peptide HA308-317) and TL3A6 (specific for myeline basic protein peptide MBP89-98) to 200 mixts. of a decapeptide PS-SCL was analyzed. The proliferative response of T cell clones to PS-SCL is analyzed by quantitating TCR recognition of antigens or autoantigens by clonotypic T cell.

L13 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2002 ACS
AN 2001:169420 CAPLUS
DN 134:338077
TI Helicobacter pylori ***strain*** -specific differences in genetic content, ***identified*** by ***microarray*** , influence host inflammatory responses
AU Israel, Dawn A.; Salama, Nina; Arnold, Carrie N.; Moss, Steven F.; Ando, Takafumi; Wirth, Hans-Peter; Tham, Kyi T.; Camorlinga, Margorita; Blaser, Martin J.; Falkow, Stanley; Peek, Richard M., Jr.
CS Division of Gastroenterology, Vanderbilt University School of Medicine, Nashville, TN, USA
SO Journal of Clinical Investigation (2001), 107(5), 611-620
CODEN: JCINAO; ISSN: 0021-9738
PB American Society for Clinical Investigation
DT Journal
LA English
AB Helicobacter pylori enhances the risk for ulcer disease and gastric cancer, yet only a minority of H. pylori-colonized individuals develop disease. The authors examd. the ability of two H. pylori isolates to induce differential host responses in vivo

or in vitro was examd. and then an H. pylori whole-genome ***microarray*** was used to identify ***bacterial*** determinants related to pathogenesis. Gastric ulcer strain B128 induced more severe gastritis, proliferation, and apoptosis in gerbil mucosa than did duodenal ulcer strain G1.1, and gastric ulceration and atrophy occurred only in B128+ gerbils. In vitro, gerbil-passaged B128 derivs. significantly increased IL-8 secretion and apoptosis compared with G1.1 strains. ***DNA*** hybridization to the ***microarray*** ***identified*** several ***strain*** -specific differences in gene compn. including a large deletion of the cag pathogenicity island in strain G1.1. Partial and complete disruption of the cag island in strain B128 attenuated induction of IL-8 in vitro and decreased gastric inflammation in vivo. Thus, the ability of H. pylori to regulate epithelial cell responses related to inflammation depends on the presence of an intact cag pathogenicity island. Use of an H. pylori whole-genome ***microarray*** is an effective method to identify differences in gene content between H. pylori strains that induce distinct pathol. outcomes in a rodent model of H. pylori infection.
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s l1 and l5
L14 12 L1 AND L5

=> s l14 not l13

L15 9 L14 NOT L13

=> d l15 1-9 bib ab

L15 ANSWER 1 OF 9 CAPLUS COPYRIGHT 2002 ACS
AN 2002:507943 CAPLUS
TI Dissection of a complex phenotype by functional genomics reveals roles for the yeast cyclin-dependent protein kinase Pho85 in stress adaptation and cell integrity
AU Huang, Dongqing; Moffat, Jason; Andrews, Brenda
CS Department of Medical Genetics and Microbiology, University of Toronto, Toronto, ON, M5S 1A8, Can.
SO Molecular and Cellular Biology (2002), 22(14), 5076-5088
CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB Cyclin-dependent kinases (Cdks) are key regulators of the cell division cycle. Pho85 is a multifunctional Cdk in budding yeast involved in aspects of metab., the cell cycle, cell polarity, and gene expression. Consistent with a broad spectrum of functions, Pho85 assocs. with a family of 10 cyclins and deletion of PHO85 causes a pleiotropic phenotype. Discovering the physiol. substrates of protein kinases is a major challenge, and we have pursued a no. of genomics approaches to reveal the processes regulated by Pho85 and to understand the root cause of reduced cellular fitness in pho85.DELTA. mutant strains. We used a functional-genomics approach called synthetic genetic array (SGA) anal. to systematically ***identify*** ***strain*** backgrounds in which PHO85 is required for viability. In parallel, we used ***DNA*** ***microarrays*** to examine the genome-wide transcriptional consequences of deleting PHO85 or members of the Pho85 cyclin family. Using this pairwise approach coupled with phenotypic tests, we uncovered clear roles for Pho85 in cell integrity and the response to adverse growth conditions. Importantly, our combined approach allowed us to ascribe new aspects of the complex pho85 phenotype to particular cyclins; our data highlight a cell integrity function for the Pcl1,2 subgroup of Pho85 Cdks that is independent of a role for the Pho80-Pho85 kinase in the response to stress. Using a modification of the SGA technique to screen for suppressors of pho85.DELTA. strain growth defects, we found that deletion of putative vacuole protein gene VTC4 suppressed the sensitivity of the pho85.DELTA. strain to elevated CaCl2 and many other stress conditions. Expression of VTC4 is regulated by Pho4, a transcription factor that is inhibited by the Pho80-Pho85 kinase. Genetic tests and electron microscopy expts. suggest that VTC4 is a key target of Pho4 and that Pho80-Pho85-mediated regulation of VTC4 expression is required for proper vacuole function and for yeast cell survival under a variety of suboptimal conditions. The integration of multiple genomics approaches is likely to be a generally useful strategy for extg. functional information from pleiotropic mutant phenotypes.
RE.CNT 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 2 OF 9 CAPLUS COPYRIGHT 2002 ACS
AN 2002:426199 CAPLUS
DN 137:51873
TI Using ***DNA*** ***microarrays*** to identify strains and species of Cryptosporidium
AU Straub, Timothy M.; Chandler, Darrell P.; Rochelle, Paul A.; De Leon, Ricardo
CS Battelle Memorial Institute - Northwest, Richland, WA, 99352, USA
SO Proceedings - Water Quality Technology Conference (2001) 2106-2114 CODEN: PWQCD2; ISSN: 0164-0755
PB American Water Works Association
DT Journal; (computer optical disk)
LA English
AB Mol. biol. methods have been developed to rapidly identify Cryptosporidium sp. in water supplies. PCR primers targeting the heat shock 70 protein can specifically amplify C. parvum from other Cryptosporidium species, but distinguishing between human and animal strains requires further mol. typing methods. The primary benefit of strain typing Cryptosporidium parvum isolates lies in the ability to perform risk characterization studies to inform utilities of potential watershed issues or infrastructure problems. ***DNA*** ***microarrays*** may offer a powerful tool to ***identify*** Cryptosporidium ***strain*** and species isolates that can bridge the gap between detection for regulatory purposes and detection for epidemiol. investigation. Essentially a miniaturized version of a reverse dot blot, ***microarrays*** can interrogate thousands of sites within a single gene or across multiple genes of the same organism. Using image anal. software, differences down to a single base pair mismatch can be statistically achieved. In this study, the authors designed a prototype 68 probe ***microarray*** to achieve single and double nucleotide mismatch discrimination of 7 variable positions within a 190 bp region of the C. parvum hsp70 gene. PCR was used to generate biotin or fluorescently labeled probes to hybridize to the array. Initial results with two genotype I strains and two genotype II strains indicated that the array could easily distinguish between these two genotypes. Single and double nucleotide mismatch discrimination was also possible using Cy3 labeled PCR products, but achieving this was limited by the yield of PCR products. Future studies will include other Cryptosporidium isolates and refinement of the array to address other variable regions within the hsp70 gene and other diagnostic genes. These initial developments may provide utilities with addnl. new and simple methods for assessing sources and types of C. parvum in watersheds.
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 3 OF 9 CAPLUS COPYRIGHT 2002 ACS
AN 2002:72338 CAPLUS
DN 136:113786
TI Identification of renal protective factor genes associated with renal injury and their use in diagnosis and treatment of diseases
IN Raha, Debasish; Green, Cyndi D.; Cates, Richard L.
PA Curagen Corporation, USA; Biogen, Inc.
SO PCT Int. Appl., 67 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---- ---------- ---- -------- ---------- --------
PI WO 2002006537 A2 20020124 WO 2001-US41374 20010713
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 2002142284 A1 20021003 US 2001-905325 20010713
PRAI US 2000-217932P P 20000713
AB Disclosed are methods of identifying toxic agents, e.g., renal toxic agents, using differential RPF (renal protective factor) gene expression in a subject. Also disclosed are novel RPF nucleic acid sequences whose expression is differentially regulated by renal injury agents. A method for detg. susceptibility to renal injury by comparing RPF differential gene expression in test cell populations contacted with said test agent and ref. populations is disclosed. The said test cell populations can be mouse or human and the test agent can be administered in vivo or in vitro. Gene expression of at least 5 or more RFP genes treated with toxic agents were compared. Diseases assocd. with renal injury are ischemic kidney injury, renal transplantation, drug toxicity, cancer, diabetes, hypertension, childhood lupus nephritis and polycystic kidney disease. ***DNA*** ***microarrays*** and kits for detecting RPF gene expression and methods of treating a renal disorder by modulating RPF gene expression.

L15 ANSWER 4 OF 9 CAPLUS COPYRIGHT 2002 ACS
AN 2001:688793 CAPLUS
DN 136:274173
TI Chipping away at complex behavior: Transcriptome/phenotype correlations in the mouse brain
AU Carter, T. A.; Del Rio, J. A.; Greenhall, J. A.; Latronica, M. L.; Lockhart, D. J.; Barlow, C.
CS Laboratory of Genetics, The Salk Institute for Biological Studies, La Jolla, CA, 92037, USA
SO Physiology & Behavior (2001), 73(5), 849-857 CODEN: PHBHA4; ISSN: 0031-9384
PB Elsevier Science Inc.
DT Journal
LA English
AB Highly parallel gene expression profiling has the potential to provide new insight into the mol. mechanisms of complex brain diseases and behavioral traits. We review how gene expression profiling in various brain regions of inbred mouse strains has been used to ***identify*** genes that may contribute to ***strain*** -specific phenotypes. New data, which demonstrate the use of gene expression profiling in combination with behavioral testing to identify candidate genes involved in mediating variation in running wheel activity, are also presented. These and other studies suggest that a combination of gene expression profiling and more traditional genetic approaches, such as quant. trait locus anal., can be used to identify genes responsible for specific neurobehavioral phenotypes.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 5 OF 9 CAPLUS COPYRIGHT 2002 ACS
AN 2001:562851 CAPLUS
DN 136:227319
TI Post genome analysis of Campylobacter jejuni
AU Wren, B. W.; Linton, D.; Dorrell, N.; Karlyshev, A. V.
CS Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, WC1E 7HT, UK
SO Society for Applied Microbiology Symposium Series (2001), 30(Campylobacter, Helicobacter and Arcobacter), 36S-44S CODEN: SMSSFP; ISSN: 0267-4440
PB Blackwell Science Ltd.
DT Journal; General Review
LA English
AB A review that focuses on describing three major findings from analyzing the Campylobacter jejuni ***strain*** NCTC11168 genome sequence, including the ***identification*** of over 24 hypervariable genes, a novel capsule locus, and multiple sialic acid biosynthetic pathways (genes neuB, neuB1 and neuB2). The authors also speculate on the impact of post genomic anal. on the study of C. jejuni, with particular emphasis on the application of a C. jejuni ***DNA*** ***microarray*** . Completion of the C. jejuni NCTC11168 genome sequence offers unrivaled opportunities to understand the mol. basis of virulence for this major pathogen. Among the many novel features revealed by the genome sequence are at least 24 hypervariable sequences mostly found in genes encoding surface structures. Variation in the length of poly G/C tracts in genes contg. these hypervariable sequences is frequently found in other mucosal pathogens and is likely to play a key role in enabling C. jejuni to evade the host immune response. Addnl., a novel capsule locus and three sialylation pathways were identified which may be important in the pathogenesis of both uncomplicated diarrheal disease and neurol. sequelae of infection. The availability of the C. jejuni genome sequence data has coincided with important technol. advances in bioinformatics, gene mutagenesis, proteome anal. and ***DNA*** ***microarrays*** . A C. jejuni ***DNA*** ***microarray*** holds great promise for transcriptome and comparative genome anal. Given the range of disease assocd. with C. jejuni infection, combined with the diverse genotypic and phenotypic properties of clin. and environmental isolates, a Campylobacter ***DNA*** ***microarray*** will be particularly useful in detg. correlates of pathogenicity and in deciphering the epidemiol. of the organism. Post genome studies will liberate our understanding of C. jejuni from the piecemeal study of individual genes or operons towards a comprehensive anal. of the entire gene and protein complement. Armed with this wealth of new information, the opportunities to develop improved intervention strategies to reduce C. jejuni in the food chain will be enormous.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 6 OF 9 CAPLUS COPYRIGHT 2002 ACS
AN 2001:476006 CAPLUS
DN 136:145608
TI Functional genomics of Mycobacterium tuberculosis using ***DNA*** ***microarrays***
AU Wilson, Michael; Voskuil, Martin; Schnappinger, Dirk; Schoolnik, Gary K.
CS Affymax Research Institute, Santa Clara, CA, USA
SO Methods in Molecular Medicine (2001), 54(Mycobacterium tuberculosis Protocols), 335-357 CODEN: MMMEFN
PB Humana Press Inc.
DT Journal; General Review
LA English

AB A review with refs. discusses the fabrication and use of a Mycobacterium tuberculosis ***microarray*** , contg. representations of each of the identified 3924 open reading frames (ORFs) of this organism. The two applications of this method are described: the ***microarray*** -based gene response (transcript profiling) and comparative genomics. In the latter, a ***microarray*** contg. the ORFs of one ***strain*** or species was used to ***identify*** ORFs deleted or absent from a second strain or species whose genome sequence may not have been detd. In this manner, ***microarray*** -based comparative genomics seeks to learn the ORF-by-ORF relatedness of two similar, but non-identical organisms whose biol. differences are under study. Examples of each application have been applied to M. tuberculosis.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 7 OF 9 CAPLUS COPYRIGHT 2002 ACS
AN 2001:352232 CAPLUS
DN 134:348942
TI Recombinant yeast providing arrays used for screening agents specifically targeting heterologous genes
IN Dawson, Dean; Swindle, John
PA Complegen, Inc., USA
SO U.S., 18 pp. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---- ---------- ---- -------- ---------- --------
PI US 6232074 B1 20010515 US 1999-459752 19991210 WO 2001042446 A2 20010614 WO 2000-US33329 20001208 WO 2001042446 A3 20011129 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG EP 1242593 A2 20020925 EP 2000-984067 20001208 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRAI US 1999-459752 A 19991210 WO 2000-US33329 W 20001208
AB This invention relates to functional gene arrays of yeast. Novel aspects include the individual yeast cells, methods for making the yeast and the arrays, and uses for the arrays. A diploid bearing special genetic properties has been constructed to facilitate cloning of heterologous genes capable of providing essential functions. A selection method, using this ***strain*** allows the ***identification*** haploid yeast strains dependent for life on heterologous essential genes. The arrays of these strains comprise a library of unique members where each member is dependent for survival on the function of a heterologous gene complementing a different essential host gene which has been inactivated by the insertion of a dominant selectable marker. These arrays provide screening platforms for agents that specifically target the activity of these heterologous genes.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 8 OF 9 CAPLUS COPYRIGHT 2002 ACS
AN 2001:323609 CAPLUS
DN 134:306053
TI A survey of the Leishmania major Friedlin strain V1 genome by shotgun sequencing: a resource for DNA microarrays and expression profiling
AU Akopyants, N. S.; Clifton, S. W.; Martin, J.; Pape, D.; Wylie, T.; Li, L.; Kissinger, J. C.; Roos, D. S.; Beverley, S. M.
CS Department of Molecular Microbiology, Washington University School of Medicine, St. Louis, MO, USA
SO Molecular and Biochemical Parasitology (2001), 113(2), 337-340 CODEN: MBIPDP; ISSN: 0166-6851
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Genomic DNA was isolated from Leishmania major strain Friedlin clone V1 (MHOM/JL/80/Friedlin) and a total of 10,314 sequences were characterized by random shotgun sequencing. Database comparisons showed that 971 (9.4%) of the genome survey sequences (GSS) contain various repetitive elements such as telomeric and subtelomeric repeats. About 7543 sequences (73.1%) lacked obvious similarity to any protein sequence in GenBank, while 1800 (17.5%) showed significant similarities. To facilitate gene identification, the GSS sequences were combined with 1281 genomic cosmid or PAC end sequences and 2191 ESTs previously deposited in GenBank, an addnl. 2972 unpublished end sequences, and other Leishmania data available from GenBank to create a single BLAST-queryable database which can be found at http://paradb.cis.upenn.edug/leish/index.html. This database is well suited for expression profiling studies. [This abstr. record is the second of 2 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

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AN 2001:239188 CAPLUS
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TI A survey of the Leishmania major Friedlin strain V1 genome by shotgun sequencing: a resource for DNA microarrays and expression profiling
AU Akopyants, N. S.; Clifton, S. W.; Martin, J.; Pape, D.; Wylie, T.; Li, L.; Kissinger, J. C.; Roos, D. S.; Beverley, S. M.
CS Department of Molecular Microbiology, Washington University School of Medicine, St. Louis, MO, USA
SO Molecular and Biochemical Parasitology (2001), 113(2), 337-340 CODEN: MBIPDP; ISSN: 0166-6851
PB Elsevier Science Ireland Ltd.
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